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**PROGRAM,  
BOOK OF ABSTRACTS,  
AUTHOR INDEX.**

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## Social insect intestines are mating nests for *Saccharomyces cerevisiae*

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Sex can be a difficult task for motionless dispersed organisms such as the yeast *Saccharomyces cerevisiae*. Albeit yeasts are known to mainly asexually reproduce in nature, they should rely on sex to generate new genetic assemblies. Recent studies on the worldwide *S. cerevisiae* wild biodiversity significantly broadened the yeast population genetics horizons. Nevertheless, indication on where the yeast sexual reproduction can occur is still lacking. Social insects, by vectoring and maintaining yeast cells in the wild and among different environments, guarantee a possible site for yeasts meeting and mating. *S. cerevisiae* strains isolated from the intestines of social insects show higher heterozygosity than any other wild and human-related isolate, indicating an occurred genome mixing of different yeast lineages. We provide experimental evidence that *Saccharomyces sensu stricto* strains co-habiting the intestines of social insects can face sexual reproduction, generating inter- and intra-specific hybrids. This indication, rising from the identification and whole-genome sequencing of *S. cerevisiae* X *S. paradoxus* and *S. cerevisiae* X *S. bayanus* hybrids isolated from the wild *V. crabroguts*, is mirrored by results obtained in *in vitro* conditions (*Polistes* spp. and *Apis mellifera*). The intestine of social insects is identified as the niche where *Saccharomyces* spp. can meet and mate, finally acting as yeasts mating nest and contributing in shaping the fungal evolutionary ecology.

## Evolution of complex microbial communities for biotransformation of tar produced by biomass pyrolysis

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Biomass is an important alternative to fossil fuels, for energy production through pyrolysis and gasification. However, this thermo-chemical process leads to the formation of toxic condensable compounds (tar) mainly composed by polycyclic aromatic hydrocarbons (PAH) and volatile monocyclic aromatic compounds (BTEX). Up to now the problem of the disposal of tar from biomass gasification is far to be solved. Bioremediation of tar with a mixed microbial culture despite its complexity seems a highly promising and innovative approach for the handling of these byproducts. Microbial resource management is a new concept dealing with the use of complex bacterial and fungal communities to achieve a particular objective, such as xenobiotic degradation or mineralization. The evolution concept is at the basis of this new approach, since microbiologists can benefit of the genetic and physiologic adaptation of the living bacteria and fungi when inoculated in adverse environments. The aim of this study is to assess the degradation dynamics of three different laboratory-scale microcosms enriched with complex tars, where natural microbial consortia are used for the treatment of tars. Tars were incubated with a complex microbial consortium taken from highly polluted soils. Triplicate microcosms were setup and incubated at room temperature for 30 days. Aliquots were taken at different time intervals to assess the structure and diversity of the biodegrading bacterial communities by Denaturing Gradient Gel Electrophoresis (DGGE), Automated Ribosomal Intergenic Spacer Analysis (ARISA) and 16S rRNA gene pyrotagging. Chemical analyses were carried out by GC/MS before and after microbial growth. For all the different tars, bacterial growth could be observed after two days. However, tar color changed visibly only after 6 days. Both the bacterial growth and the change in color were not detected in the negative controls. At day 30, all the inoculated microcosms were completely odorless, whereas the negative controls emitted the characteristic tar scent as intensively as at day 0. This sensory perception was confirmed by chemical analysis as a proof of the occurred degradation of the volatile fraction. ARISA reliability of replicated microcosms was very high (97%). ARISA electropherograms and 16S rRNA gene pyrotagging confirmed that a bacterial consortia was growing and evolving in the degrading microcosms, and it was for sure feeding on tar since tar was the only carbon source available. Bacterial species grew accordingly to a “cross-feeding” behavior, involving the use of metabolic outputs of one species as an energy source for another one. The evolution of the microbial consortia and of single microbial taxa during all the time points will be presented at the conference